

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 8, 2001, 16:29:17 ; Search time 13.59 Seconds

(without alignments)  
190.577 Million cell updates/sec

Title: US-09-447-800-1

Sequence: 1 XVEIQLMHNIGKILSMEREWLRKKLDVHNF 34

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR,68:\*

1: p1r1:\*\*\*  
2: p1r2:\*\*\*  
3: p1r3:\*\*\*  
4: p1r4:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	115	1	PTHU
2	168	95.5	115	1	PTHU
3	167	94.9	115	1	PTHU
4	167	94.9	115	2	JC4202
5	158	89.8	115	2	A05091
6	150	85.2	105	2	I51851
7	121	68.8	119	2	A34937
8	61	34.7	824	2	F72408
9	58	33.0	175	1	JN0103
10	58	33.0	177	1	PTHU2L
11	58	33.0	177	1	A30012
12	58	33.0	177	2	JC4201
13	58	33.0	209	1	PTHU3L
14	56	31.8	115	2	H72705
15	35	31.2	94	2	T09450
16	35	31.2	94	2	C64559
17	54	30.7	176	1	SI0202
18	54	30.7	564	2	T38291
19	54	30.7	564	2	T43298
20	54	30.7	1257	1	I58383
21	54	30.7	2470	2	S57085
22	52	29.5	363	2	F70195
23	51.5	29.3	508	1	A43713
24	51.5	29.3	528	2	D65214
25	51.5	29.3	528	2	C86099
26	51.5	29.3	560	2	C41539
27	51.5	29.3	569	2	I53013
28	51	29.0	336	2	F84056
29	51	29.0	611	2	S38162

nucleotides

30	51	29.0	752	1	C2HU	complement C2 prec
31	51	29.0	764	1	BBHU	complement factor
32	51	29.0	1038	2	T15098	hypothetical prote
33	51	29.0	2182	2	T14320	calcineurin inhibi
34	51	29.0	2479	1	MNWVRA	nonstructural poly
35	50.5	28.7	145	2	E84938	flagellar flid pro
36	50.5	28.7	3394	2	T18501	hypothetical prote
37	50	28.4	91	1	C64069	virulence-associat
38	50	28.4	570	2	G72595	hypothetical prote
39	50	28.4	722	2	B86583	transcription elon
40	50	28.4	722	2	C72040	transcription elon
41	50	28.4	2473	1	S38040	1-phosphatidylinos
42	50	28.4	3678	2	S28916	dystrophin - mouse
43	49.5	28.1	339	2	T18926	hypothetical prote
44	49.5	28.1	490	1	S71776	calcium-dependent
45	49.5	28.1	564	1	HMTWC2	hemagglutinin prec

#### ALIGNMENTS

RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: proparathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence-revision 19-Jan-1996 #text-change 08-Dec-2000

C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410;

R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr.

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <VAS>

A:Cross-references: GB:J00301; NID:q190702; PIDN:AA60215.1; PID:q190704

R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of mepirin from human kidney and its role in parathyroid hormone

A:Reference number: S53790; MUID:95225988

A:Accession: S53790

A:Molecule type: Protein

A:Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>

A>Note: peptides generated in vitro and in vivo by mepirin; peptide cleavage also occu

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human proparathyroid hormone by a new microsequencing

A:Reference number: A93169; MUID:74174967

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <JAC>

R:Olsstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik,

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylated for

action.

A:Reference number: S21199; MUID:92209518

A:Accession: S21199

A:Molecule type: Protein

A:Residues: 32-114,'N' <OLS>

A>Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylati

R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyro

A:Reference number: A93789; MUID:74111656

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residue

A:Reference number: A93783; MUID:73070429

A:Accession: A93783

A:Molecule type: protein

A:Residues: 32-52,'O',54-58,'K',60,'L',62-65 <BRE>  
 A:Note: this sequence was determined by sequenator and mass spectroscopic identification  
 R:Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.  
 Biochemistry 14, 1842-1847, 1975  
 A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.  
 A:Reference number: A90387; MUID:75146516  
 A:Accession: A90387  
 A:Molecule type: protein  
 A:Residues: 52-75 <KE3>  
 R:Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.  
 Biochemistry 17, 5723-5729, 1978  
 A:Title: Complete amino acid sequence of human parathyroid hormone.  
 A:Reference number: A90426; MUID:79082855  
 A:Accession: A90426  
 A:Molecule type: protein  
 A:Residues: 61-106,'D',108-115 <KEU>  
 R:Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H.;  
 in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-10  
 A:Reference number: A94410  
 A:Accession: A94410  
 A:Molecule type: protein  
 A:Residues: 75-100 <KE2>  
 R:Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.  
 Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974  
 A:Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone.  
 A:Reference number: A91660; MUID:75059220  
 A:Contents: annotation; synthesis of residues 32-65  
 A:Note: the biologically active amino-terminal 34 residues of parathyroid hormone were synthesized at renal adenylate cyclase assay and with the bovine hormone's active region in the chick  
 R:Andreatta, R.H.; Hartmann, A.; Joehel, A.; Kamber, B.; Maier, R.; Riniker, B.; Ritttel, H.  
 Helv. Chim. Acta 56, 470-473, 1973  
 A:Title: Synthese der Sequenz 1-34 von menschlichem Parathormon.  
 A:Reference number: A91635; MUID:73227467  
 A:Contents: annotation; synthesis of residues 32-65  
 A:Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroiddecomized rats caused a distinct increase in plasma calcium level  
 R:Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981  
 A:Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.  
 A:Reference number: 138342; MUID:82150870  
 A:Accession: 138342  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-115 <RES>  
 A:Cross-references: EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID:g37144  
 C:Genetics:  
 A:Gene: GDB:PTH  
 A:Cross-references: GDB:119522; OMIM:168450  
 A:Map position: 11p15.2-11p15.1  
 A:Introns: 29/2  
 A:Note: the first intron occurs before the initiator codon  
 C:Function:  
 A:Description: factor in homeostatic control of plasma calcium and phosphate; released by parathyroid gland  
 C:Superfamily: parathyroid hormone; parathyroid hormone homology  
 C:Keywords: calcium; hormone; parathyroid gland; plasma  
 F:1-25/Domain: signal sequence #status predicted <SIG>  
 F:26-31/Domain: propeptide #status experimental <PRO>  
 F:30-64/Domain: parathyroid hormone homology <PTH>  
 F:32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 100.0%; Score 176; DB 1; Length 115;  
 Best Local Similarity 97.18; Pred. No. 1.9e-15;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XVSSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 :|||||  
 Db 32 SVSSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 65

RESULT 2

PTPG

parathyroid hormone precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 24-Apr-1984 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
 A:Accession: B26806; A90390; A90376; A01535  
 R:Schmeizler, H.J.; Gross, G.; Widera, G.; Mayer, H.  
 Nucleic Acids Res. 15, 6740, 1987  
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h  
 A:Reference number: A26806; MUID:87316938  
 A:Accession: B26806  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-115 <SCH>  
 A:Cross-references: GB:X05722; GB:X00409; NID:gl838; PIDN:CAA29193.1; PID:gl839  
 R:Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.  
 Biochemistry 14, 3631-3635, 1975  
 A:Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial am  
 A:Reference number: A90390; MUID:76018954  
 A:Accession: A90390  
 A:Molecule type: protein  
 A:Residues: 26-115 <CHU>  
 R:Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr.  
 Biochemistry 13, 1994-1999, 1974  
 A:Title: The amino acid sequence of porcine parathyroid hormone.  
 A:Reference number: A90376; MUID:74253317  
 A:Accession: A90376  
 A:Molecule type: protein  
 A:Residues: 32-109 <SAU>  
 R:Brewer Jr., H.B.; Fairwell, T.; Ritttel, W.; Littledike, T.; Arnaud, C.D.  
 Am. J. Med. 56, 759-766, 1974  
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hor  
 A:Reference number: A90030; MUID:74173303  
 A:Contents: annotation  
 C:Superfamily: parathyroid hormone; parathyroid hormone homology  
 C:Keywords: calcium; hormone; parathyroid gland  
 F:1-25/Domain: signal sequence #status predicted <SIG>  
 F:26-31/Domain: propeptide #status experimental <PRO>  
 F:30-64/Domain: parathyroid hormone homology <PTH>  
 F:32-115/Product: parathyroid hormone #status experimental <MAT>  
 Query Match 95.5%; Score 168; DB 1; Length 115;  
 Best Local Similarity 91.2%; Pred. No. 1.9e-14;  
 Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XVSSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 :|||||  
 Db 32 SVSSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 65  
 RESULT 3  
 PTBO  
 parathyroid hormone precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 18-Jun-1999  
 A:Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534  
 R:Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.  
 Gene 28, 319-329, 1984  
 A:Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroi  
 A:Reference number: A24949; MUID:84262483  
 A:Accession: A24949  
 A:Molecule type: DNA  
 A:Residues: 1-115 <WEA>  
 A:Cross-references: GB:K01938  
 R:Kronenberg, H.M.; McDewitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979  
 A:Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid h  
 A:Reference number: A93835; MUID:80056617  
 A:Accession: A93835  
 A:Molecule type: DNA  
 A:Residues: 1-115 <KRO>  
 A:Cross-references: GB:V00106; GB:J00023; NID:g84; PIDN:CAA23439.1; PID:g85  
 A:Note: the authors translated the codon GAA for residue 50 as Gly  
 R:Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.

C:Species: Canis lupus familiaris (dog)  
C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 16-Jul-1999  
C:Accession: J04202  
R:Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.  
Gene 160, 241-243, 1995  
A:Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein A  
A:Reference number: J04201; MUID:95369696  
A:Accession: J04202  
A:Molecule type: mRNA  
A:Residues: 1-115 <ROS>  
A:Cross-references: GB:U15662; NID:g558915; PIDN:AAA82584.1; PID:g558916  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-31/Domain: signal sequence #status Predicted <SIG>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status Predicted <MAT>

Query Match 94.9%; Score 167; DB 2; Length 115;  
Best Local Similarity 91.2%; Pred. No. 2.6e-14;  
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34  
          :|||||:|||||:|||||:|||||:|||||  
Db 32 VSVEIQFMHNLGKHLNSMERVEWLKRLQDVHNF 65

RESULT 5  
A05091  
parathyroid hormone precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 16-Jul-1999  
C:Accession: A05091; A26806  
R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.  
J. Biol. Chem. 259, 3320-3329, 1984  
A:Reference number: A05091; MUID:84135845  
A:Accession: A05091  
A:Molecule type: DNA  
A:Residues: 1-115 <HEI>  
A:Cross-references: GB:X01268; NID:g206483; PIDN:AAA41979.1; PID:g206485  
A:Note: the authors translated the codon GAA for residue 87 as Asp  
R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.  
Nucleic Acids Res. 13, 6740, 1987  
A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h  
A:Reference number: A26806; MUID:87316938  
A:Accession: A26806  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-115 <SCH>  
A:Cross-references: GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29192.1; PID:g56003  
C:Genetics:  
A:Introns: 29/3  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
F:30-64/Domain: parathyroid hormone homology <PTH>

Query Match 89.8%; Score 158; DB 2; Length 115;  
Best Local Similarity 85.3%; Pred. No. 3.6e-13;  
Matches 29; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34  
          :|||||:|||||:|||||:|||||:|||||  
Db 32 AVSEIQLMHNLGKHLASVERMQLWLRKKLQDVHNF 65

RESULT 6  
I51851  
parathyroid hormone - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I51851  
R:Schmelzer, H.  
Adv. Gene Technol. 21, 228-229, 1984

A:Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.

A:Reference number: 151851

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-105 <RES>

A:Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933

C:Genetics:

A:Gene: PTH

C:Superfamily: parathyroid hormone; parathyroid hormone homology

F:20-54/Domain: parathyroid hormone homology <PTH>

Query Match 85.2%; Score 150; DB 2; Length 105;  
Best Local Similarity 79.4%; Pred. No. 3.4e-12;  
Matches 27; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 XVSEIQLMHNGLKHLNSMERVWLRKKLQDVHN 34

Db 22 AISEIQLMHNGLKHLASVERMQWLRRKLQDGHNF 55

RESULT 7

A34937

parathyroid hormone precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999

C:Accession: A34937; I50411

R:Russell, J.; Sherwood, L.M.

Mol. Endocrinol. 3, 325-331, 1989

A:Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid

A:Reference number: A34937; MUID:89219100

A:Accession: A34937

A:Molecule type: mRNA

A:Residues: 1-119 <RUS>

A:Cross-references: GB:M31604; NID:g212767; PIDN:AAA49093.1; PID:g212768

R:Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.

J. Bone Miner. Res. 3, 689-698, 1988

A:Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.

A:Reference number: I50411; MUID:89284968

A:Accession: I50411

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-119 <RUS>

A:Cross-references: GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g212592

C:Superfamily: parathyroid hormone; parathyroid hormone homology

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-31/Domain: propeptide #status predicted <PRO>

F:30-64/Domain: parathyroid hormone homology <PTH>

F:32-119/Product: parathyroid hormone #status predicted <MAT>

Query Match 68.8%; Score 121; DB 2; Length 119;  
Best Local Similarity 63.6%; Pred. No. 1.9e-08;  
Matches 21; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 XVSEIQLMHNGLKHLNSMERVWLRKKLQDVHN 33

Db 32 SVSEQLMHNGLGEHRTVERQDQLMKLQDVHS 64

RESULT 8

F72408

leucine--tRNA ligase (EC 6.1.1.4) - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C:Accession: F72408

R:Neilson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

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A:Residues: 176-177 <YAS2>

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

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A:Residues: 176-177 <YAS2>

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

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A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

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A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

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A:Molecule type: DNA

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A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

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A:Molecule type: DNA

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A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

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A:Molecule type: DNA

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A:Accession: B33360

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A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360

A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

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A:Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712

A:Molecule type: DNA

A:Residues: 176-177 <YAS2>

A:Accession: B33360



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Query Match          31.8%; Score 56; DB 2; Length 115;
Best Local Similarity 42.9%; Pred. No. 3.4;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY      1  XVEGIOLMHNGLGRHLNSMERVEWLRKKL 28
      :|: : :| | | | | | | | | | | | | |
Db       17  EVAALYILHRLGPTLNYGEAVETLRERL 44

RESULT 15
T09450
virulence-associated protein D - Helicobacter pylori (strain 60190)
C:Species: Helicobacter pylori
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09450
R:Caio, P.; Cover, T.L.
J. Bacteriol. 179, 2852-2856, 1997
A:Title: High-level genetic diversity in the vapD chromosomal region of Helicobacter pylori
A:Reference number: Z16675; MUID:97284485
A:Accession: T09450
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-94 <CAO>
A:Cross-references: EMBL:U94318; NID:g2072451; PIDN:AAC45241.1; PID:g2072452
C:Genetics:
A:Gene: vapD
C:Superfamily: virulence-associated protein vapD
C:Keywords: virulence

Query Match          31.2%; Score 55; DB 2; Length 94;
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Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

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      | : | : : | | : | : | : |
Db       59  KAIKLSQIEWFKASVRDIRAF 80

Search completed: August 8, 2001, 16:30:06
Job time: 49 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 8, 2001, 16:29:17 ; Search time 10.12 seconds  
(without alignments)  
115.088 Million cell updates/sec

Title: US-09-447-800-1

Perfect score: 176

Sequence: 1 XVSEIQLMHNHLGKLNLMERWLRKKLQDVHNF 34

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	176	100.0	115	1 PTHY_HUMAN	P01270 homo sapien
2	176	100.0	115	1 PTH_WACFA	Q9xt35 macaca fasc
3	168	95.5	115	1 PTHY_PIG	P01269 sus scrofa
4	167	94.9	115	1 PTHY_BOVIN	P01268 bos taurus
5	167	94.9	115	1 PTHY_CANFA	P52212 canis fami
6	158	89.8	115	1 PTHY_RAT	P04089 rattus norv
7	121	68.8	119	1 PTHY_CHICK	P15743 gallus gall
8	61	34.7	824	1 SYL_THEMA	Q9wy15 thermotoga
9	58	33.0	175	1 PTHR_MOUSE	P22858 mus musculu
10	58	33.0	177	1 PTHR_CANFA	P52211 canis fami
11	58	33.0	177	1 PTHR_HUMAN	P12272 homo sapien
12	58	33.0	177	1 PTHR_RAT	P13085 rattus norv
13	55	31.2	94	1 VAPD_HELPY	O05728 helicobacte
14	54	30.7	176	1 PTHR_CHICK	P17251 gallus gall
15	54	30.7	176	1 PTHR_MOUSE	P17251 gallus gall
16	54	30.7	1257	1 RBFL_HUMAN	Q10134 schizosacch
17	54	30.7	2470	1 TOR1_YEAST	P29374 homo sapien
18	52	29.5	363	1 MURG_BORBU	P35169 saccharomyc
19	51.5	29.3	508	1 CDPK_SOYBN	O51708 borrelia bu
20	51.5	29.3	528	1 YJCC_ECOLI	P28583 glycine max
21	51.5	29.3	556	1 KNLK_RAT	P32701 escherichia
22	51.5	29.3	569	1 KNLK_HUMAN	P32785 rattus norv
23	51	29.0	611	1 HBS1_YEAST	Q07866 homo sapien
24	51	29.0	752	1 CO2_HUMAN	P32769 saccharomyc
25	51	29.0	764	1 CFAB_HUMAN	P06681 homo sapien
26	51	29.0	2182	1 CAB1_RAT	P00751 homo sapien
27	51	29.0	2479	1 POLN_RRVN	O88480 rattus norv
28	50.5	28.7	145	1 FLIJ_BUCAL	P13887 ross river
29	50	28.4	89	1 VAP1_RIEN	P57179 buchera ap
30	50	28.4	91	1 VAPD_HAEIN	O85172 riemerella
31	50	28.4	722	1 GREA_CHLPN	P71351 haemophilus
32	50	28.4	2473	1 TOR2_YEAST	Q92794 chlamydia p
33	50	28.4	3678	1 DMD_MOUSE	P32600 saccharomyc
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RESULT	PTHY_HUMAN	STANDARD	PRT	115 AA
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DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH) (PARATHORMONE).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=82150870; PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=83169834; PubMed=6220408;			
RA	Vasicek T.J., McDevitt B.E., Freeman M.W., Fennick B.J.,			
RT	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RL	"Nucleotide sequence of the human parathyroid hormone gene."			
RP	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RP	SEQUENCE OF 26-37.			
RP	MEDLINE=74174967; PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	"Structural analysis of human parathyroid hormone by a new			
RL	microsequencing approach."			
RP	Nature 249:155-157(1974).			
RP	SEQUENCE OF 32-68.			
RP	MEDLINE=74111656; PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RT	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RL	"The amino-acid sequence of the amino-terminal 37 residues of human			
RP	parathyroid hormone."			
RP	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RP	SEQUENCE OF 61-83 AND 84-115.			
RP	MEDLINE=79082855; PubMed=728431;			
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
RT	Potts J.T. Jr.;			
RL	"Complete amino acid sequence of human parathyroid hormone."			
RP	Biochemistry 17:5723-5729(1978).			
RP	SEQUENCE OF 75-100.			
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,			
RT	O'Riordan J.L.H., Potts J.T. Jr.;			
RL	(In) Talmadge R.V., Owen M., Parsons J.A. (eds.);			
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,			
RL	Amsterdam (1975).			

O46673 orcinus orc  
Q09217 caenorhabdi  
P09345 influenza a  
P04507 reovirus (t  
P33225 escherichia  
Q09733 schizosacch  
Q92m99 helicobacte  
O25116 helicobacte  
P87506 influenza a  
P25348 saccharomyc  
P21814 ovis aries  
P16171 bacillus sp

## ALIGNMENTS

hatched



[7]  
RP REVISIONS.  
RX MEDLINE=75146516; PubMed=1125201;  
RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "A reinvestigation of the amino-terminal sequence of human  
RL parathyroid hormone";  
RN Biochemistry 14:1842-1847(1975).  
[8]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE=75059220; PubMed=4474131;  
RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,  
RX Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "Solid-phase synthesis of the biologically active N-terminal 1-34  
RL peptide of human parathyroid hormone";  
RN Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).  
[9]  
RP SYNTHESIS OF 32-65.  
RX MEDLINE=73227467; PubMed=4721748;  
RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,  
RA Riniker B., Rittel W., Sieber P.;  
RT "Synthesis of sequence 1-34 of human parathyroid hormone";  
RN Helv. Chim. Acta 56:470-473(1973).  
[10]  
RP STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=91299748; PubMed=2069952;  
RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;  
RT "Investigation of the solution structure of the human parathyroid  
RL hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,  
RT and molecular dynamics calculations";  
RN Biochemistry 30:6936-6942(1991).  
[11]  
RP STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=93345518; PubMed=8344299;  
RA Barden J.A., Cuthbertson R.M.;  
RT "Stabilized NMR structure of human parathyroid hormone(1-34).";  
RN Eur. J. Biochem. 215:315-321(1993).  
[12]  
RP STRUCTURE BY NMR OF 32-68.  
RX MEDLINE=95318084; PubMed=7797503;  
RA Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,  
RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,  
RA Roesch P.;  
RT "Structure of human parathyroid hormone 1-37 in solution.";  
RN J. Biol. Chem. 270:15194-15202(1995).  
[13]  
RP STRUCTURE BY NMR OF 32-70.  
RX MEDLINE=20090619; PubMed=10623601;  
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;  
RT "Solution structures of human parathyroid hormone fragments  
RL hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment  
RL bPTH(1-37).";  
RN Biochem. Biophys. Res. Commun. 267:213-220(2000).  
[14]  
RP VARIANT ARG-18.  
RX MEDLINE=91009811; PubMed=2212001;  
RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,  
RA Kronenberg H.M.;  
RT "Mutation of the signal peptide-encoding region of the  
RL preproparathyroid hormone gene in familial isolated  
RL hypoparathyroidism";  
RN J. Clin. Invest. 86:1084-1087(1990).  
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
CC -!- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED  
CC HYPOPARATHYROIDISM (FIH).  
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
CC  
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CC  
DR EMBL; J00301; AAA60215.1;  
DR EMBL; V00597; CAA23843.1;  
DR EMBL; A29146; CAA01956.1;  
DR PIR; A01536; PTHU.  
DR PIR; A19339; A19339.  
DR PDB; 1HPH; 10-JUL-95.  
DR PDB; 1HTH; 15-OCT-97.  
DR PDB; 12WA; 12-MAR-97.  
DR PDB; 12WB; 12-MAR-97.  
DR PDB; 12WD; 12-MAR-97.  
DR PDB; 12WE; 12-MAR-97.  
DR PDB; 12WF; 16-JUN-97.  
DR PDB; 12WG; 16-JUN-97.  
DR PDB; 1BWX; 14-JAN-00.  
DR PDB; 1HPY; 14-JAN-00.  
DR MIM; 146200;  
DR MIM; 168450;  
DR InterPro; IPR001415;  
DR Pfam; PF01279; Parathyroid; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW Hormone; Signal; Disease mutation; 3D-structure.  
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FT PROPEP 26 31  
FT CHAIN 32 115  
FT VARIANT 18 18  
FT  
FT CONFLICT 107 107  
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Best Local Similarity 97.1%; Pred. No. 4.2e-16;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 32 SVSVEIOLMNLGKHLNSMERVEWLKKLQDVHNF 65  
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DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
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GN PTH.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Malaivijitnond S., Takenaka O.;  
RT "Nucleotide sequences of parathyroid gene in five species of macaque  
RT of Thailand";  
RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).  
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
CC  
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CC -----
DR EMBL; AF130257; AAD2777.1; -.
DR HSSP; P01270; IHPY.
DR InterPro; IPR001415; -.
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE597 CRC64;

Query Match 100.0%; Score 176; DB 1; Length 115;
Best Local Similarity 97.1%; Pred. No. 4.2e-16;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XVSIEQLMHNGLKHLNSMERVEWLKRLQDVHNF 34
Db 32 SVSIEQLMHNGLKHLNSMERVEWLKRLQDVHNF 65

RESULT 3
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AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine preproparathyroid hormone. Identification, biosynthesis, and
partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP SEQUENCE OF 32-115.
RX MEDLINE=74253317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA Potts J.T. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RL Biochemistry 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
-----
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-----
DR EMBL; X05722; CAA29193.1; -.
DR PIR; A01535; PTFG.
DR PIR; B26806; B26806.
DR HSSP; P01270; IHPH.
DR InterPro; IPR001415; -.

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DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;

Query Match 95.5%; Score 168; DB 1; Length 115;
Best Local Similarity 91.2%; Pred. No. 4.5e-15;
Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XVSIEQLMHNGLKHLNSMERVEWLKRLQDVHNF 34
Db 32 SVSIEQLMHNGLKHLNSMERVEWLKRLQDVHNF 65

RESULT 4
PTHY_BOVIN
ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80056617; PubMed=388425;
RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA Potts J.T. Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
at the 5' terminus of the sense strand of bovine parathyroid hormone
cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=83105964; PubMed=6185374;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84262483; PubMed=6086460;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
parathyroid hormone.";
RL Gene 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine preproparathyroid
hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE=71076162; PubMed=5531031;
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,

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RA Aurbach G.D., Potts J.T. Jr.;
RT "The amino acid sequence of bovine parathyroid hormone I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE=71063634; PubMed=5275384;
RA Brewer H.B. Jr., Ronan R.;
RT "Bovine parathyroid hormone: amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE=71091588; PubMed=4322265;
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RT Defetos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT "Synthesis of a biologically active N-terminal tetraoctapeptide
of parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN [9]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=20090619; PubMed=10623601;
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
bPTH(1-37).";
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; V00106; CAA23439.1; -
DR EMBL; J00024; AAA30747.1; -
DR EMBL; K01938; AAA30749.1; -
DR EMBL; M25082; AAA30748.1; -
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PDB; 1ZWC; 12-MAR-97.
DR InterPro; IPR001415; -
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal; 25 BY SIMILARITY.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;
CC -----
Query Match 94.9%; Score 167; DB 1; Length 115;
Best Local Similarity 91.2%; Pred. No. 6.1e-15;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 XVSEIQLMHNKGLHNSMERVEWLKKLQDVHNF 34
Db 32 AVSEIQFMHNLKGLHLSMERVEWLKKLQDVHNF 65
RESULT 5
PTHY_CANFA
ID PTHY_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.

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OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Parathyroid;
RX MEDLINE=95369696; PubMed=7642102;
RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
RA DeWille J.W., Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
protein and parathyroid hormone.";
RL Gene 160:241-243(1995).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; U15662; AAA82584.1; -
DR HSSP; P01270; 1ZWC.
DR InterPro; IPR001415; -
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal; 25 BY SIMILARITY.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;
CC -----
Query Match 94.9%; Score 167; DB 1; Length 115;
Best Local Similarity 91.2%; Pred. No. 6.1e-15;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 XVSEIQLMHNKGLHNSMERVEWLKKLQDVHNF 34
Db 32 SVSEIQFMHNLKGLHLSMERVEWLKKLQDVHNF 65
RESULT 6
PTHY_RAT
ID PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84135846; PubMed=6321505;
RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone.";
RL J. Biol. Chem. 259:3320-3329(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmeizler H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";

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RL Nucleic Acids Res. 15:6740-6740(1987).  
[3]  
RP SEQUENCE OF 10-115 FROM N.A.  
RN TISSUE-Parathyroid;  
RC Schmelzer H.J., Gross G., Mayer H.;  
RA "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid  
RT hormone.";  
FT Adv. Gene Technol. 21:228-229(1984).  
[4]  
RP SEQUENCE OF 32-115 FROM N.A.  
RN STRAIN-SPRAGUE-DAWLEY; TISSUE=Brain, Parathyroid, and Liver;  
RC MEDLINE=96079910; PubMed=7588314;  
RA Nutley M.T., Parimi S.A., Harvey S.;  
RT "Sequence analysis of hypothalamic parathyroid hormone messenger  
RN ribonucleic acid.";  
RP Endocrinology 136:5600-5607(1995).  
RN -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
CC -!- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.  
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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CC  
DR EMBL; K01268; AAA41979.1; -  
DR EMBL; X05721; CAA29192.1; -  
DR EMBL; M54875; AAA57156.1; -  
DR EMBL; S80127; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A05091; A05091.  
DR PIR; A26806; A26806.  
DR HSP; P01270; I2WB.  
DR InterPro; IPR001415; -  
DR Pfam; PF01279; Parathyroid; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW Hormone; Signal.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 115 PARATHYROID HORMONE.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 119 PARATHYROID HORMONE.  
SQ SEQUENCE 115 AA; 12722 MW; 7B434CFC528B230 CRC64;  
  
Query Match 89.8%; Score 158; DB 1; Length 115;  
Best Local Similarity 85.3%; Pred. No. 8.8e-14;  
Matches 29; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 XVSIEQLMHNGLKHLNSMERVEWLKRLQDVHNF 34  
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DB 32 AVSEIQLMHNGLKHLASVERQWLKRLQDVHNF 65  
:|||||  
  
RESULT 7  
PTHY\_CHICK  
ID PTHY\_CHICK STANDARD; PRT; 119 AA.  
AC P15743;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE PARATHYROID HORMONE PRECURSOR (PTH).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=89219100; PubMed=2710135;  
RA Russell J., Sherwood L.M.;  
RT "Nucleotide sequence of the DNA complementary to avian (chicken)  
RT preproparathyroid hormone mRNA and the deduced sequence of the  
RT hormone precursor.";  
RL Mol. Endocrinol. 3:325-331(1989).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89284968; PubMed=3251402;  
RA Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,  
RA Kronenberg H.M.;  
RT "Nucleotide sequence of cloned cDNAs encoding chicken  
RT preproparathyroid hormone.";  
RL J. Bone Miner. Res. 3:689-698(1988).  
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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CC  
DR EMBL; M31604; AAA49093.1; -  
DR EMBL; M36522; AAB02866.1; -  
DR PIR; A34937; A34937.  
DR HSP; P01270; I2WA.  
DR InterPro; IPR001415; -  
DR Pfam; PF01279; Parathyroid; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW Hormone; Signal.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 119 PARATHYROID HORMONE.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 119 PARATHYROID HORMONE.  
SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;  
  
Query Match 68.8%; Score 121; DB 1; Length 119;  
Best Local Similarity 63.6%; Pred. No. 5.3e-09;  
Matches 21; Conservative 9; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 XVSIEQLMHNGLKHLNSMERVEWLKRLQDVHNF 33  
:|||||  
DB 32 SVSEMQLMHNGLGHRHTVERQDWLQKLDVHNS 64  
:|||||  
  
RESULT 8  
SYL\_THEMA  
ID SYL\_THEMA STANDARD; PRT; 824 AA.  
AC Q9WY15;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).  
GN LEUS OR TM0168.  
OS Thermotoga maritima.  
OC Bacteria; Thermotogales; Thermotoga.  
OX NCBI\_TaxID=2336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MSB8 / DSM 3109;  
RX MEDLINE=99287316; PubMed=10360571;  
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
RA McDonald L., Utterback T.R., Melek J.A., Linher K.D., Garrett M.M.,  
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
RT "Evidence for lateral gene transfer between Archaea and Bacteria from







```
CC -!- FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS A
CC HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
CC MILK.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
CC EMBL; X52131; CAA36376.1; -
CC PIR; S10202;
CC InterPro; IPR001415; -
CC Pfam; PF01279; Parathyroid; 1.
CC PROSITE; PS00335; PARATHYROID; 1.
CC Calcium; Hormone; Signal.
CC SIGNAL
CC 1
CC FT PROPEP ? 37
CC CHAIN 38 176 PARATHYROID HORMONE-RELATED PROTEIN.
CC SEQUENCE 176 AA; 20226 MW; 60C8AB30ACF5293B CRC64;
CC
CC Query Match 30.7%; Score 54; DB 1; Length 176;
CC Best Local Similarity 34.4%; Pred. No. 3.4;
CC Matches 11; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
CC
CC QY 1 XVSEIQLMHNLGKHLNSMERVEWLKRLQDVH 32
CC DB 38 AVSEHQLLHDKGKSTQDLRRRIFLQNLIEGVN 69
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CC RESULT 15
CC GAF2_SCHPO STANDARD; PRT; 564 AA.
CC AC Q10134;
CC DT 01-FEB-1996 (Rel. 33, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
CC DE GAF2 PROTEIN (GAF-2).
CC GN GAF2 OR SPAC23E2.01.
CC OS Schizosaccharomyces pombe (Fission yeast).
CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
CC OC Schizosaccharomycetes.
CC OX NCBI_TaxID=4896;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Hoe K.-L., Park S.-K., Yoo O.-J.J., Yoo H.-S.;
CC RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC RP [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=972;
CC RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
CC RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC CC -!- SIMILARITY: BELONGS TO THE GATA-TYPE TRANSCRIPTION FACTOR FAMILY.
CC -----
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CC -----
CC EMBL; L29051; AAB38022.1; -
CC EMBL; Z68887; CAA93113.1; -
CC HSSP; P17429; 5GAT.
CC InterPro; IPR000679; -
CC Pfam; PF00320; GATA; 2.
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DR PRINTS; PR00619; GATAZNFINGER.
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 2.
DR PROSITE; PS00114; GATA_ZN_FINGER_2; 2.
KW Transcription regulation; DNA-binding; Zinc-finger; Nuclear protein.
FT ZN_FING 12 36 GATA-TYPE (BY SIMILARITY).
FT ZN_FING 172 196 GATA-TYPE (BY SIMILARITY).
FT CONFLICT 182 182 L -> K (IN REF. 1).
SQ SEQUENCE 564 AA; 60611 MW; 0ED74CE0B6E210B7 CRC64;
CC
CC Query Match 30.7%; Score 54; DB 1; Length 564;
CC Best Local Similarity 47.6%; Pred. No. 12;
CC Matches 10; Conservative 5; Mismatches 4; Indels 2; Gaps 1;
CC
CC QY 5 IOLMHNLGKHLNSMERVEWLK 25
CC DB 519 IOELHNLNHOIQID--EWLR 537
CC
CC Search completed: August 8, 2001, 16:30:41
CC Job time: 84 sec
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DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE PREPROPARATHYROID HORMONE PRECURSOR.
GN PTH.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT "Molecular cloning of feline preproparathyroid hormone.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309967; AAC30545.1; -.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 115 AA; 12921 MW; 80CD557CC6A1A47E CRC64;

Query Match 90.9%; Score 160; DB 6; Length 115;
Best Local Similarity 85.3%; Pred. No. 4.3e-13;
Matches 29; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XVSEIQLMHNIGKHLNSMERVEWLKKLQDVHNF 34
Db 32 SVSEIQFMHNIGKHLSSVERVEWLKKLQDVHNF 65

RESULT 3
Q920L6 PRELIMINARY; PRT; 115 AA.
AC Q920L6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR.
GN PTH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Karaplis A.C., He B., Hion-Tim F.F.T., Al-Akad B., Kronenberg H.M.;
RT "Cloning of the murine gene encoding parathyroid hormone: genomic
organization and nucleotide sequence.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF066075; AAC99656.1; -.
DR HSSP; P01270; 12WB.
DR InterPro; IPR001415; -.
DR InterPro; IPR003625; -.
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR SMART; SM00087; PTH; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 115 AA; 12825 MW; DA43FABBCB4E2FD9 CRC64;

Query Match 88.6%; Score 156; DB 11; Length 115;
Best Local Similarity 82.4%; Pred. No. 1.4e-12;
Matches 28; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XVSEIQLMHNIGKHLNSMERVEWLKKLQDVHNF 34
Db 32 AVSEIQLMHNIGKHLASMERQWLKKLQDMHNF 65

RESULT 4
Q918E9 PRELIMINARY; PRT; 163 AA.
AC Q918E9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR.
GN PTHRP.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20314478; PubMed=10854780;
RA Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
RA Elgar G., Clark M.S.;
RT "Genomic structure and expression of parathyroid hormone-related
protein in a teleost, Fugu rubripes.";
RL Gene 250:67-79(2000).
DR EMBL; AJ249391; CAB94712.1; -.
DR InterPro; IPR001415; -.
DR Pfam; PF01279; Parathyroid; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 163 AA; 18698 MW; 3AC5F2C764732278 CRC64;

Query Match 44.3%; Score 78; DB 13; Length 163;
Best Local Similarity 46.9%; Pred. No. 0.015;
Matches 15; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 XVSEIQLMHNIGKHLNSMERVEWLKKLQDVH 32
Db 38 SVSHAQLMHDKGRSLQEFRRRWLKLLEEVH 69

RESULT 5
Q918U2 PRELIMINARY; PRT; 162 AA.
AC Q918U2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR.
GN PTHLH.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20304721; PubMed=10843788;
RA Flanagan J.A., Power D.M., Bendall L.A., Guerreiro P.M., Fuentes J.,
RA Clark M.S., Canario A.V.M., Danks J.A., Brown B.L., Ingleton P.M.;
RT "Cloning of the cDNA for sea bream (Sparus aurata) Parathyroid
hormone-related protein.";
RL Gen. Comp. Endocrinol. 118:373-382(2000).
DR EMBL; AF197904; AAF79073.1; -.
DR InterPro; IPR001415; -.
DR InterPro; IPR003571; -.
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00206; -.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 162 AA; 18722 MW; 6E8D5E07F95EDC9 CRC64;

Query Match 42.6%; Score 75; DB 13; Length 162;
Best Local Similarity 43.8%; Pred. No. 0.036;

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db 37 AVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIH 68
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QY 14 HLNSMERVEWLKKLQDVHNF 34
Db 773 NMNSTERISFLOEKLEIRKY 793

RESULT 10
Q15992
AC Q15992; PRELIMINARY; PRT; 866 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE RETINOBLASTOMA BINDING PROTEIN I ISOFORM II (FRAGMENT).
GN RBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93205410; PubMed=8455946;
RA Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
RT "Alternative splicing of the RBP1 gene clusters in an internal exon
RT that encodes potential phosphorylation sites.";
RL Oncogene 8:949-957(1993).
DR EMBL; S57160; AAB25834.1; -
DR InterPro; IPR000953; -
DR InterPro; IPR001606; -
DR Pfam; PF01388; ARID.1; -
DR SMART; SM00298; CHROMO; 1.
FT NON_TER 1
SQ SEQUENCE 866 AA; 98332 MW; 2DCFA7A8CE06B125 CRC64;

Query Match 30.7%; Score 54; DB 4; Length 866;
Best Local Similarity 38.1%; Pred. No. 95;
Matches 8; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 14 HLNSMERVEWLKKLQDVHNF 34
Db 788 NMNSTERISFLOEKLEIRKY 808

RESULT 11
Q15991
AC Q15991; PRELIMINARY; PRT; 920 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE RETINOBLASTOMA BINDING PROTEIN I ISOFORM I (FRAGMENT).
GN RBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93205410; PubMed=8455946;
RA Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
RT "Alternative splicing of the RBP1 gene clusters in an internal exon
RT that encodes potential phosphorylation sites.";
RL Oncogene 8:949-957(1993).
DR EMBL; S57153; AAB25833.1; -
DR InterPro; IPR001606; -
DR Pfam; PF01388; ARID; 1.
DR SMART; SM00501; BRIGHT; 1.
FT NON_TER 1
SQ SEQUENCE 920 AA; 104589 MW; BD37B5F59009570A CRC64;

Query Match 30.7%; Score 54; DB 4; Length 920;

QY 14 HLNSMERVEWLKKLQDVHNF 34
Db 773 NMNSTERISFLOEKLEIRKY 793

RESULT 12
Q15992
AC Q15992; PRELIMINARY; PRT; 130 AA.
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-10 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046210; AAC40095.1; -
DR HSP; P22301; IINR.
DR InterPro; IPR000098; -
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR SMART; SM00188; IL10; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15260 MW; DAFE3B5FC216B380 CRC64;

Query Match 30.4%; Score 53.5; DB 11; Length 130;
Best Local Similarity 47.8%; Pred. No. 15;
Matches 11; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 13 KHLNSM-ERVEWLKKLQDVHNF 34
Db 74 EHLNSLGEKLTLLRQLQCHRF 96

RESULT 13
Q9V5W8
ID Q9V5W8 PRELIMINARY; PRT; 787 AA.
AC Q9V5W8; Q9V5W7; Q9TV63;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE LOLA PROTEIN (BTB-IV PROTEIN DOMAIN).
GN LOLA OR BTBIV OR CG12052 OR CG18376.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE DMSTPROX.  
CN MSTPROX OR CG1149.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96215042; PubMed=8621445;  
RA Mitcham J.L., Parnet P., Bonner T.P., Garika K.E., Gerhart M.J.,  
RA Slack J.L., Gayle M.A., Dower S.K., Sims J.E.;  
RT "Tl/St2 signaling establishes it as a member of an expanding  
interleukin-1 receptor family."  
RL J. Biol. Chem. 271:5777-5783(1996).  
DR EMBL; U42425; AAC46999.1; -.  
DR FlyBase; FBgn0015770; MstProx.  
DR InterPro; IPR000157; -.  
DR InterPro; IPR000372; -.  
DR InterPro; IPR001611; -.  
DR Pfam; PF00560; LRR; 2.  
DR Pfam; PF01462; LRRNT; 1.  
DR Pfam; PF01582; TIR; 1.  
DR SMART; SM00255; TIR; 1.  
SQ SEQUENCE 711 AA; 83175 MW; 007CD7AEF67BC1B0 CRC64;

Query Match 29.8%; Score 52.5; DB 5; Length 711;  
Best Local Similarity 28.6%; Pred. No. 1.2e+02;  
Matches 10; Conservative 11; Mismatches 7; Indels 7; Gaps 1;  
Qy 1 XVSEIQLMHNLCCKHLNSMERSV-----EWLRKKL 28  
Db 212 LINEPQLQSMHRKLNLTNTMSIYKYMEWLRKL 246

Search completed: August 8, 2001, 16:31:09  
Job time: 112 sec